



SEQUENCE LISTING

1

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Burkly, Linda C.

<120> TREATMENT FOR ASTHMA

<130> 10274-003003

<140> 09/251,073
<141> 1999-02-16

<150> 08/822,830
<151> 1997-03-21

<150> 08/456,193
<151> 1995-05-31

<150> 08/374,331
<151> 1995-01-18

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<150> 08/256,631
<151> 1994-07-12

<150> PCT/US93/00030
<151> 1993-01-12

<150> 07/821,768
<151> 1992-01-13

<160> 16

<170> FastSEQ for Windows Version 4.0

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<211> 363
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(363)

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gar gtc aaa ctg cag cag tct ggg gca gag ctt gtg aag cca ggg gcc
Glu Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15

48

tca gtc aag ttg tcc tgc aca gct tct ggc ttc aac att aaa gac acc
Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30

96

tat atg cac tgg gtg aag cag agg cct gaa cag ggc ctg gag tgg att
Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45

144

gga agg att gat cct gcg agt ggc gat act aaa tat gac ccg aag ttc 192
 Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe
 50 55 60

cag gtc aag gcc act att aca gcg gac acg tcc tcc aac aca gcc tgg 240
 Gln Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp
 65 70 75 80

ctg cag ctc agc agc ctg aca tct gag gac act gcc gtc tac tac tgt 288
 Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gca gac gga atg tgg gta tca acg gga tat gct ctg gac ttc tgg ggc 336
 Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly
 100 105 110

caa ggg acc acg gtc acc gtc tcc tca 363
 Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 2

<211> 121

<212> PRT

<213> Homo sapiens

<400> 2

Glu Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
 20 25 30

Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe
 50 55 60

Gln Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp
 65 70 75 80

Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly
 100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser

115 120

<210> 3

<211> 318

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(318)

<400> 3

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 Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly

1	5	10	15	
gac agg gtt acc ata acc tgc aag gcc agt cag agt gtg act aat gat				96
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp				
20	25	30		
gta gct tgg tac caa cag aag cca ggg cag tct cct aaa ctg ctg ata				144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile				
35	40	45		
tat tat gca tcc aat cgc tac act gga gtc cct gat cgc ttc act ggc				192
Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly				
50	55	60		
agt gga tat ggg acg gat ttc act ttc acc atc agc act gtg cag gct				240
Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala				
65	70	75	80	
gaa gac ctg gca gtt tat ttc tgt cag cag gat tat agc tct ccg tac				288
Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr				
85	90	95		
acg ttc gga ggg ggg acc aag ctg gag atc				318
Thr Phe Gly Gly Thr Lys Leu Glu Ile				
100	105			

<210> 4
<211> 106
<212> PRT
<213> Homo sapiens

<400> 4

Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly				
1	5	10	15	
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp				
20	25	30		
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile				
35	40	45		
Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly				
50	55	60		
Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala				
65	70	75	80	
Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr				
85	90	95		
Thr Phe Gly Gly Thr Lys Leu Glu Ile				
100	105			

<210> 5
<211> 1347
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1338)

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atg cct ggg aag atg gtc gtg atc ctt gga gcc tca aat ata ctt tgg			48
Met Pro Gly Lys Met Val Val Ile Leu Gly Ala Ser Asn Ile Leu Trp			
1 5 10 15			
ata atg ttt gca gct tct caa gct ttt aaa atc gag acc acc cca gaa			96
Ile Met Phe Ala Ala Ser Gln Ala Phe Lys Ile Glu Thr Thr Pro Glu			
20 25 30			
tct aga tat ctt gct cag att ggt gac tcc gtc tca ttg act tgc agc			144
Ser Arg Tyr Leu Ala Gln Ile Gly Asp Ser Val Ser Leu Thr Cys Ser			
35 40 45			
acc aca ggc tgt gag tcc cca ttt ttc tct tgg aga acc cag ata gat			192
Thr Thr Gly Cys Glu Ser Pro Phe Phe Ser Trp Arg Thr Gln Ile Asp			
50 55 60			
agt cca ctg aat ggg aag gtg acg aat gag ggg acc aca tct acg ctg			240
Ser Pro Leu Asn Gly Lys Val Thr Asn Glu Gly Thr Thr Ser Thr Leu			
65 70 75 80			
aca atg aat cct gtt agt ttt ggg aac gaa cac tct tac ctg tgc aca			288
Thr Met Asn Pro Val Ser Phe Gly Asn Glu His Ser Tyr Leu Cys Thr			
85 90 95			
gca act tgt gaa tct agg aaa ttg gaa aaa gga atc cag gtg gag atc			336
Ala Thr Cys Glu Ser Arg Lys Leu Glu Lys Gly Ile Gln Val Glu Ile			
100 105 110			
tac tct ttt cct aag gat cca gag att cat ttg agt ggc cct ctg gag			384
Tyr Ser Phe Pro Lys Asp Pro Glu Ile His Leu Ser Gly Pro Leu Glu			
115 120 125			
gct ggg aag ccg atc aca gtc aag tgt tca gtt gct gat gta tac cca			432
Ala Gly Lys Pro Ile Thr Val Lys Cys Ser Val Ala Asp Val Tyr Pro			
130 135 140			
ttt gac agg ctg gag ata gac tta ctg aaa gga gat cat ctc atg aag			480
Phe Asp Arg Leu Glu Ile Asp Leu Leu Lys Gly Asp His Leu Met Lys			
145 150 155 160			
agt cag gaa ttt ctg gag gat gca gac agg aag tcc ctg gaa acc aag			528
Ser Gln Glu Phe Leu Glu Asp Ala Asp Arg Lys Ser Leu Glu Thr Lys			
165 170 175			

agt ttg gaa gta acc ttt act cct gtc att gag gat att gga aaa gtt			576
Ser Leu Glu Val Thr Phe Thr Pro Val Ile Glu Asp Ile Gly Lys Val			
180 185 190			
ctt gtt tgc cga gct aaa tta cac att gat gaa atg gat tct gtg ccc			624
Leu Val Cys Arg Ala Lys Leu His Ile Asp Glu Met Asp Ser Val Pro			
195 200 205			
aca gta agg cag gct gta aaa gaa ttg caa gtc gac aaa act cac aca			672
Thr Val Arg Gln Ala Val Lys Glu Leu Gln Val Asp Lys Thr His Thr			
210 215 220			

tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc ttc Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe 225	230	235	240	720
ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cg acc cct Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro 245	250		255	768
gag gtc aca tgc gtg gtg gac gtg agc cac gaa gac cct gag gtc Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val 260	265		270	816
aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr 275	280		285	864
aag ccg cgg gag gag cag tac aac agc acg tac cgg gtg gtc agc gtc Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val 290	295		300	912
ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys 305	310	315	320	960
aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser 325	330		335	1008
aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro 340	345		350	1056
tcc cgg-gat-gag ctg acc aag-aac cag-gtc agc ctg-acc-tgc-ctg gtc Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val 355	360		365	1104
aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly 370	375		380	1152
cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp 385	390	395	400	1200
ggc tcc-ttc-ttc-ctc tac agc aag-ctc-acc gtg-gac-aag-agc-agg tgg Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp 405	410		415	1248
cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His 420	425		430	1296
aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys 435	440		445	1338
tgagtgcgg				1347

<210> 6
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 6
tcgtcgacaa aactcacaca tgcc

24

<210> 7
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 7
gttaaatgagt gcggcggccg ccaa

24

<210> 8
<211> 115
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 8
gcggccgccc tccaaccacc aatctcaaag cttggtagcc gggattcag atctgcagca
tgctcgagct ctatatatcg attccatgga tcctcacatc ccaatccgatg gccgc

60

115

<210> 9
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 9
gagtcgagg cggccgcacc atgcctggaa agatggtcgt g - - - - - 41 - - - - -

<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 10
aagtgcactt gcaattcttt tac

23

<210> 11
 <211> 14
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 11
 tcgacgcggc cgcg 14

<210> 12
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 <213> Homo sapiens

<220>
 <221> CDS
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 Gln Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
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tca gtc aag ttg tcc tgc aca gct tct ggc ttc aac att aaa gac acc 96
 Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
 20 25 30

tat atg cac tgg gtg aag cag agg cct gaa cag ggc ctg gag tgg att 144
 Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45

gga agg att gat cct gcg agt ggc gat act aaa tat gac ccg aag ttc 192
 Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe
 50 55 60

cag gtc aag gcc act att aca gcg gac acg tcc tcc aac aca gcc tgg 240
 Gln Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp
 65 70 75 80

ctg cag ctc agc acg ctg aca tct gag gac act gcc gtc tac tac tgt 288
 Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

gca gac gga atg tgg gta tca acg gga tat gct ctg gac ttc tgg ggc 336
 Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly
 100 105 110

caa ggg acc acg gtc acc gtc tcc tca 363
 Gln Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 13
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 <212> PRT

<213> Homo sapiens

<400> 13
Gln Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
20 25 30
Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
35 40 45
Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe
50 55 60
Gln Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp
65 70 75 80
Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly
100 105 110
Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 14

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetically generated peptide

<400> 14

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1 5

<210> 15

<211> 7

<212> PRT

<213> Artificial Sequence

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<223> Synthetically generated peptide

<400> 15

Met Pro Gly Lys Met Val Val
1 5

<210> 16 - - - - -

<211> 5

<212> PRT

<213> Homo sapiens

<400> 16

Glu Ile Leu Asp Val
1 5